

SMBE 2015, Hofburg Vienna, Austria

Tentative Schedule - Overview of sessions

Colors indicate multi-session symposia.

Symposium	Organizers/Chairs
Symp1 Beyond the Equilibrium Paradigm: The role of temporal processes in population genetics and evolution	D. Balick, A. Nourmohammad
Symp2 Untangling information, noise, and phylogenetic reconstruction in genome scale data	K. W. Hilu, J. Townsend, A. RoyChoudhury
Symp3 The biological impact of transposable elements	J. González, E. Pritham
Symp4 Evolution and Ecology of microbial communities	M. Groussin, F. Lassalle
Symp5 Open Symposium	T. Hill, A.-M. Jakšić, D. Schrempf, D. Setter, R. Tobler
Symp6 Population Genomics of Rapid Adaptation	D. Petrov, P. Messer
Symp7 Origins and evolution of molecular innovation	J. Masel, R. Neme, E. Bornberg-Bauer
Symp8 The Horizontal Component of Microbial Evolution	Tal Dagan, J. Peter Gogarten
Symp9 Inference of demography and selection under violations of the Kingman coalescent assumptions	A. Tellier, T. Giraud
Symp10 Speciation genomics	P. Novikova, O. Paun
Symp11 PopGen in space! Theory and inference in spatial population genetics	J. Novembre, G. Coop
Symp12 Micro-evo-devo: using natural variation to explain the how and why of phenotypic evolution	A. McGregor, M.D.S. Nunes, L.F. Pallares
Symp13 Inferring fitness landscapes from experimental evolution	D. McCandlish, J. Plotkin
Symp14 Cancer as a Darwinian process	O. Carja, N. Creanza, L. Fogarty
Symp15 The evolution of alternative splicing	J. Roux, É. Laine, H. Richard
Symp16 Exploring the consequences of ancient and contemporary gene flow	K. Harris, T. Linderoth, J.A. Capra, C. Simonti
Symp17 Genomics of sex bias: Addressing questions with or without genomes	M.A. Wilson Sayres, J.J. Emerson
Symp18 Within- and between-host viral evolution	R.A. Goldstein, S. Hué
Symp19 Novel Functional Approaches to Evolutionary Genomics	I. Gallego Romero, N. Banovich
Symp20 Evolution of molecular pathways and networks: Molecular evolution meets systems biology	M.A. Fares, D. Alvarez-Ponce
Symp21 Fungal Evolutionary Genomics: Unravelling Mysteries from the Forgotten Kingdom	C.T. Hittinger, J. Schacherer, K. Wolfe
Symp22 Adaptive and non-adaptive evolution of gene expression and regulation	S. Laurent, J. Jensen, A. Necsulea, M. Somel
Symp23 Reframing the demography vs. selection debate using 21st century models and data	K. E. Lohmueller, E. Huerta-Sanchez
Symp24 Short Tandem Repeats in the Post-Genomics Age: Accurate Typing, Variability, Evolution, and Function	K. Makova, N. Gemmell
Symp25 Ancient Genomes: A Time Machine for Investigating Natural Selection	Z. Faltyskova, Y. Diekmann, D. Diez del Molino, P. Gerbault, M. Thomas
Symp26 Genomic and Epigenomic Evolution of Sex Chromosomes: Broad Patterns and Intriguing Cases	Qi Zhou, John Wang
Symp27 The origins of multicellularity under the light of functional genomics	A. de Mendoza, A. Sebé-Pedrós
Symp28 The golden age of Archaea: unveiling the diversity and evolution of the third Domain of Life	S. Gribaldo, C. Brochier-Armanet
Extra Symposium: NGS library construction: the frequently underestimated challenge	

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Program overview

Sunday, July 12th	
14:00-18:00	Registration
18:00-19:00	Plenary talk (at Festsaal)
19:00-23:00	Welcome Reception

Monday, July 13th					
	FESTSAAL	ZEREMONIEN-SAAL	FORUM	PRINZ EUGEN	RATSTUBE
08:15-09:15	Plenary talk (at Festsaal)				
09:15-10:45	Symp1 Beyond the Equilibrium Paradigm: The role of temporal processes in population genetics and evolution	Symp2 Untangling information, noise, and phylogenetic reconstruction in genome scale data	Symp3 The biological impact of transposable elements	Symp4 Evolution and Ecology of microbial communities	Symp5 Open Symposium
10:45-11:15	Coffee Break				
11:15-12:45	Symp1 (contin.)	Symp2 (contin.)	Symp3 (contin.)	Symp4 (contin.)	Symp5 Open Symposium
12:45-14:15	Lunch Break	13:00 – 14:00 NGS library construction: the frequently underestimated challenge	Lunch Break		
14:15-15:00	Posters A				
15:00-15:45	Posters B				
15:45-16:15	Coffee Break				
16:15-17:45	Symp6 Population Genomics of Rapid Adaptation	Symp7 Origins and evolution of molecular innovation	Symp3 (contin.)	Symp8 The Horizontal Component of Microbial Evolution	Symp5 Open Symposium
17:45-18:30	Poster A				
18:30-19:15	Poster B				
19:15-20:00	Posters C				
20:00-20:45	Posters D				
20:45-21:00	Leave the building				

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Tuesday, July 14th					
	FESTSAAL	ZEREMONIEN- SAAL	FORUM	PRINZ EUGEN	RATSTUBE
08:15-09:15	Plenary talk (at Festsaal)				
09:15-10:45	Symp6 Population Genomics of Rapid Adaptation (contin.)	Symp7 Origins and evolution of molecular innovation (contin.)	Symp9 Inference of demography and selection under violations of the Kingman coalescent assumptions	Symp8 The Horizontal Component of Microbial Evolution (contin.)	Symp5 Open Symposium
10:45-11:15	Coffee Break				
11:15-12:45	Symp10 Speciation genomics	Symp11 PopGen in space! Theory and inference in spatial population genetics	Symp12 Micro-evo-devo: using natural variation to explain the how and why of phenotypic evolution	Symp13 Inferring fitness landscapes from experimental evolution	Symp5 Open Symposium
12:45-14:15	Lunch Break	13:00 – 14:00 NGS library construction: the frequently underestimated challenge	Lunch Break		
14:15-15:00	Posters C				
15:00-15:45	Posters D				
15:45-16:15	Coffee Break				
16:15-17:45	Symp10 (contin.)	Symp11 (contin.)	Symp14 Cancer as a Darwinian process	Symp13 (contin.)	Symp15 The evolution of alternative splicing
17:45-18:00	Leave the building				

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Wednesday, July 15th

	FESTSAAL	ZEREMONIEN- SAAL	FORUM	PRINZ EUGEN	RATSTUBE
08:15– 10:30	Fitch Symposium (at Festsaal)				
10:30- 11:15	Coffee Break				
11:15– 12:45	Symp16 Exploring the consequences of ancient and contemporary gene flow	Symp11 PopGen in space! Theory and inference in spatial population genetics (contin.)	Symp17 Genomics of sex bias: Addressing questions with or without genomes	Symp18 Within- and between-host viral evolution	Symp19 Novel Functional Approaches to Evolutionary Genomics
12:45- 14:15	Lunch Break with posters	13:00 – 14:00 NGS library construction: the frequently underestimated challenge	Lunch Break with posters		
14:15– 15:45	Symp16 (contin.)	Symp20 Evolution of molecular pathways and networks: Molecular evolution meets systems biology	Symp17 (contin.)	Symp18 (contin.)	Symp21 Fungal Evolutionary Genomics: Unravelling Mysteries from the Forgotten Kingdom
15:45- 16:15	Coffee Break				
16:15– 17:45	Symp22 Adaptive and non-adaptive evolution of gene expression and regulation	Symp20 (contin.)	Symp23 Reframing the demography vs. selection debate using 21st century models and data	Symp24 Short Tandem Repeats in the Post-Genomics Age: Accurate Typing, Variability, Evolution, and Function	Symp21 (contin.)
17:45- 18:00	Leave the building				

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Thursday, July 16th

	FESTSAAL	ZEREMONIEN- SAAL	FORUM	PRINZ EUGEN	RATSTUBE
08:15-10:45	Symp22 Adaptive and non-adaptive evolution of gene expression and regulation (contin.)	Symp7 Origins and evolution of molecular innovation (contin.)	Symp23 Reframing the demography vs. selection debate using 21st century models and data (contin.)	Symp25 Ancient Genomes: A Time Machine for Investigating Natural Selection	Symp26 Genomic and Epigenomic Evolution of Sex Chromosomes: Broad Patterns and Intriguing Cases
10:45-11:15	Coffee Break				
11:15-12:45	Symp22 (contin.)	Symp10 Speciation genomics (contin.)	Symp1 Beyond the Equilibrium Paradigm: The role of temporal processes in population genetics and evolution (contin.)	Symp2 Untangling information, noise, and phylogenetic reconstruction in genome scale data (contin.)	Symp27 The origins of multicellularity under the light of functional genomics
12:45-14:15	Lunch Break with posters (Take down posters at the end)				
14:15-15:45	Symp22 (contin.)	Symp6 Population Genomics of Rapid Adaptation (contin.)	Symp11 PopGen in space! Theory and inference in spatial population genetics (contin.)	Symp 20 Evolution of molecular pathways and networks: Molecular evolution meets systems biology (contin.)	Symp28 The golden age of Archaea: unveiling the diversity and evolution of the third Domain of Life
15:45-16:15	Coffee Break				
16:15-17:45	Final Plenary Talk, Announcement of Prizes, Next Year's SMBE (at Festsaal)				
17:45-18:00	Leave the building				

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Detailed Program:

Sunday, July 12th

Time	
14:00-18:00	Registration (Hofburg Foyer)
18:00-19:00	Plenary Talk: Pl.1 in Festsaal How natural selection may connect evolutionary biology to physics <i><u>Joseph Felsenstein</u></i>
19:00-23:00	Welcome Reception (Hofburg Foyer & Seitengalerie)

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Early morning, Monday, July 13th

Time	Festsaal	Zeremoniensaal	Forum
8:15-9:15	Plenary Talk: PI.2 <i>De novo</i> evolution of genes <u>Diethard Tautz</u>		
	1 Beyond the Equilibrium Paradigm: The role of temporal processes in population genetics and evolution	2 Untangling information, noise, and phylogenetic reconstruction in genome scale data	3 The biological impact of transposable elements
09:15	1.1 Adaptive immunity and predictability of evolution in commensal gut bacteria <u>J. Barroso-Batista, J. Demengeot, Isabel Gordo</u>	2.1 Analytical and computational challenges in coalescent-based species tree estimation <u>Tandy Warnow, S. Mirarab, M. Bayzid, B. Boussau</u>	3.1 SIRT6 represses LINE1 retrotransposons by ribosylating KAP1 but this repression fails with stress and age <u>M. Meter, M. Kashyap, R. Sarallah, A. Geneva, T. Morello, A. Seluanov, Vera Gorbunova</u>
09:45	1.2 Characterising the within-host fitness landscape of the influenza virus using time-resolved sequence data <u>Chris Illingworth</u>	2.2 Species tree inference with polymorphism-aware phylogenetic models <u>Dominik Schrempf, N. Maio, C. Kosiol</u>	3.2 Transposable elements contribute to rapid adaptation in interspecific hybrids <u>Caiti Smukowski Heil, M. Dunham</u>
10:00	1.3 Evolutionary dynamics of an optimal adaptive immune response <u>Tobias Lenz</u>	2.3 Statistical inference of reticulate evolutionary histories <u>Luay Nakhleh, Y. Yu, J. Dong, J. Degnan, K. Liu</u>	3.3 Frequency and impact of horizontal transfer of transposable elements from moth to virus <u>Clément Gilbert, J. Peccoud, A. Chateigner, E. Herniou, R. Cordaux</u>
10:15	1.4 Risk and reward of high mutation rate: why large populations favor mutators while small populations inhibit them. <u>Scott Wylie, Y. Raynes, P. Sniegowski, D. Weinreich</u>	2.4 Approximate likelihood estimation of divergence time range in population trees using a coalescent-based model <u>Arindam RoyChoudhury</u>	3.4 Activities and Biological Impact of Mobile Elements in Canines <u>Julia Wildschutte, A. Doucet, R. Wayne, C. Vila, T. Marquès-Bonet, A. Boyko, J. Moran, J. Kidd</u>
10:30	1.5 Genomic variation across space and time in <i>Drosophila simulans</i> and <i>D. melanogaster</i> <u>Heather Machado, A. Bergland, E. Behrman, K. O'Brien, P. Schmidt, D. Petrov</u>	2.5 Partition-aware tree testing <u>Heiko Schmidt, F. Stertz</u>	3.5 Exploring the phenotypic space and the evolutionary history of a natural mutation in <i>Drosophila melanogaster</i> <u>Anna Ullastres, N. Petit, J. González</u>
10:45-11:15	Coffee Break		

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Early morning, Monday, July 13th

Time	Prinz Eugen	Ratstube	Notes
8:15-9:15	Plenary Talk 2 (in Festsaal)		
	4 Evolution and Ecology of microbial communities	5 Open Symposium	
09:15	4.1 Towards understanding microbial communities: From gut to ocean <u>Peer Bork</u>	5.1 Genomics of adaptation and species cohesion in ecologically divergent forest trees (Populus spp.) <u>Margot Paris, K. Stölting, C. Meier, B. Heinze, S. Castiglione, D. Bartha, D. Sanz, S. Gonzalez-Martinez, C. Lexer</u>	
09:45	4.2 Host genetic variation at B4galnt2 influences intestinal microbial ecology and susceptibility to enteric pathogens in house mice <u>John Baines, P. Rausch, M. Vallier, A. Suwandi, J. Johnsen, G. Grassl</u>	5.18 Enhancing Reproducibility in Bioinformatics for Microbiology <u>Paul Walsh, B. Kelly, M. Bekaert, R. Sleator, J. Carroll, X. Lu</u>	
10:00	4.3 Invasions of the Pharynx: Microbiome of Infected Respiratory Tissue <u>Asha Ram, U. Ijaz, C. Quince, T. Evans, J. Lindström</u>	5.3 From genome to function: Timing adaptations in the intertidal insect <i>Clunio marinus</i> <u>Tobias S. Kaiser</u>	
10:15	4.4 Rapid changes in the gut microbiome during human evolution <u>Andrew Moeller, B. Hahn, A. Pusey, H. Ochman</u>	5.4 Genomic imprinting and its systematic perturbation in abortive interspecific tomato seeds <u>A. Florez-Rueda, M. Paris, A. Schmidt, A. Widmer, U. Grossniklaus, Thomas Städler</u>	
10:30	4.5 The landscape of epistasis in natural bacterial populations <u>Daniel Falush</u>	5.5 Joint estimation of contamination, sequencing error and demography for nuclear DNA from ancient humans <u>Fernando Racimo, G. Renaud, M. Slatkin</u>	
10:45-11:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Late morning, Monday, July 13th

Time	Festsaal	Zeremoniensaal	Forum
	1 Beyond the Equilibrium Paradigm (contin.)	2 Untangling information, noise, and phylogenetic reconstruction in genome scale data (contin.)	3 The biological impact of transposable elements (contin.)
11:15	1.6 Recent evolution of the mutation rate and spectrum in Europeans <i>Kelley Harris</i>	2.6 Speed Dating with Least Squares <i>T. To, M. Jung, S. Lycett, Olivier Gascuel</i>	3.6 Transposon landscape dynamics and the evolution of Piwi-interacting RNA (piRNA) Clusters. <i>R. Rahman, G. Chim, Y. Syntnikova, J. Matts, M. Zeng, D. Gerlach, M. Yu, B. Berger, B. Kile, Nelson Lau</i>
11:30	1.7 Beyond 2/3--1/3: time-dependence of the signature of sex-biased admixture on the X chromosome <i>Amy Goldberg, N. Rosenberg</i>		
11:45	1.8 Efficient inference of time-varying population demography and locus-specific mutation rates from large-sample genomic variation data <i>Anand Bhaskar, R. Wang, Y. Song</i>	2.7 Using a phylogenetic approach to investigate genomic evolution <i>K Jun Tong, S. Duchene, C. Foster, N. Lo, S. Ho</i>	3.7 The evolutionary consequences of piRNA-mediated epigenetic silencing of transposable elements in <i>Drosophila melanogaster</i> <i>Grace Yuh Chwen Lee</i>
12:00	1.9 Demographic-aware inference of the strength of purifying selection based on haplotype patterns <i>Diego Ortega Del Vecchyo, K. Lohmueller, J. Novembre</i>	2.8 LS ³ : A data subselection algorithm to reduce long branch attraction artifact in multi-gene phylogenies <i>Carlos J. Rivera-Rivera, J. Montoya-Burgos</i>	3.8 Transposable elements continuously remodel the regulatory landscape of mammalian endometrial stromal cells <i>Vincent Lynch</i>
12:15	1.10 Background selection with non-equilibrium demographic models <i>Ryan Hernandez</i>	2.9 A whole-genome phylogenetic hypothesis across the three domains of life <i>Rebecca Dikow</i>	3.9 Does the presence of transposable elements near genes impact epigenetic modifications and gene expression in human? <i>A. Haudry, L. Gregoire, Emmanuelle Lerat</i>
12:30	1.11 Analysing Evolve and Resequencing Experiments <i>Srdjan Sarikas, K. Bodova, N. Barton</i>	2.10 Gene mode of evolution, phylogenetic informativeness and tree structure: A study in land plants <i>Khidir Hilu</i>	3.10 Co-option of endogenous retroviral envelope proteins in the convergent evolution of the fish placenta <i>Nathaniel Jue, R. O'Neill, M. O'Neill</i>
12:45-14:15	Lunch Break	13:00 – 14:00 NGS library construction: the frequently underestimated challenge Lexogen: RNA-Seq	

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Late morning, Monday, July 13th

Time	Prinz Eugen	Ratstube	Notes
	4 Evolution and Ecology of microbial communities (contin.)	5 Open Symposium	
11:15	4.6 Genomic diversification in the bacterial gut symbionts of social bees <u>Nancy Moran</u>	5.6 Human adaptation to life in the high arctic <u>Ida Moltke, M. Fumagalli, N. Grarup, F. Racimo, P. Bjerregaard, M. Jørgensen, T. Komeliussen, P. Gerbault, E. Huerta-Sanchez, O. Pedersen, T. Hansen, A. Albrechtsen, R. Nielsen</u>	
11:45	4.7 Unorthodox transmission modes of endosymbionts in hybrids and the symbiotic origin of speciation <u>Wolfgang Miller, D. Schneider, L. Ehrman</u>	5.7 Strong cis-regulation of allele-specific DNA methylation in jewel wasp reciprocal F1 hybrids <u>Xu WANG, J. Werren, A. Clark</u>	
12:00	4.8 Ecology and evolution of deep sea coral-associated bacterial communities <u>Iliana Baums, R. Dannenberg, D. Ruiz, S. Vohsen, C. Fisher</u>	5.8 A small impact of generation times on mutation rates in apes <u>Carlos Eduardo G. Amorim, P. Moorjani, Z. Gao, M. Wyman, M. Przeworski</u>	
12:15	4.9 Temporal scales in the study of microbial ecology and evolution. <u>Purificacion Lopez-Garcia, M. Simon, D. Moreira, P. Deschamps, G. Restoux, P. Bertolino, L. Jardillier</u>	5.9 Human coding RNA editing is generally nonadaptive <u>Jianzhi Zhang</u>	
12:30	4.10 Coevolution of Gene Expression Across 322 Marine Microbial Species <u>Trevor Martin, H. Fraser</u>	5.10 A genomic study of the contribution of DNA methylation to regulatory evolution in primates <u>Julien Roux, H. Irene, N. Banovich, R. Perez, C. Chavarria, A. Mitrano, J. Pritchard, T. Marques-Bonet, Y. Gilad</u>	
12:45-14:15	Lunch Break, library construction talks in Zeremoniensaal		

SMBE 2015, Hofburg Vienna, Austria

Late afternoon and Evening, Monday, July 13th

Time	Festsaal	Zeremoniensaal	Forum
14:15		Poster Session: Posters A	
15:00		Poster Session: Posters B	
15:45-16:15		Coffee Break	
	6 Population Genomics of Rapid Adaptation	7 Origins and evolution of molecular innovation	3 The biological impact of transposable elements (contin.)
16:15	6.1 Rapid evolutionary response to climate change in an ecologically important invertebrate <i>Thomas Bataillon, G. Nicolas, A. Bernard, N. Cryer, N. Faivre, S. Santoni, D. Severac, T. Mikkelsen, K. Larsen, C. Beier, J. Sørensen, M. Holmstrup, B. Ehlers</i>	7.1 The link between pervasive transcription and de novo gene evolution <i>J. Ruiz-Orera, J. Villanueva-Cañas, M. Mar Albà</i>	3.11 ALU exaptation enriches protein repertoire by introducing poly(A) signals <i>Eitan Lavi, L. Carmel</i>
16:30			3.12 The impact of social lifestyle on the repetitive elements landscapes in ten bee genomes - a case of social immunity? <i>Eckart Stolle, Kraus, Kraus, S. Helbing, R. Moritz</i>
16:45	6.2 Predicting Carriers of Ongoing Selective Sweeps with the Haplotype Allele Frequency (HAF) score <i>R. Ronen, G. Tesler, A. Akbari, S. Zakov, N. Rosenberg, Vineet Bafna</i>	7.2 Transcription of primate-specific endogenous retrovirus ERVH creates new genes and defines human naïve-like stem cells. <i>J. Wang, G. Xie, M. Singh, A. Ghanbarian, T. Rasko, A. Szvetnik, H. Cai, D. Besser, A. Proigione, N. Fuchs, G. Schumann, W. Chen, M. Lorincz, Z. Ivivs, Z. Izsvak, Laurence Hurst</i>	3.13 Evolution of structural variation in a hybrid species of Cottus <i>Stefan Dennenmoser, A. Nolte</i>
17:00	6.3 Characterizing adaptive evolution in <i>Drosophila melanogaster</i> through the patterns of incomplete selective sweeps detected by composite likelihood ratio, extended haplotype, and other summary statistic-based methods <i>Ha My Vy Thi, Y. Kim</i>	7.3 New domains as actors of molecular innovation: physico-chemical properties, evolutionary analyses and origination <i>Tristan Bitard-Feildel, S. Klasberg, M. Heberlein, I. Callebaut, E. Bornberg-Bauer</i>	3.14 Massive bursts of transposable element activity in <i>Drosophila</i> <i>Robert Kofler, V. Nolte, C. Schlötterer</i>
17:15	6.4 The evolution of dispersal-related traits in invasive cane toads <i>Lee Rollins, M. Richardson, J. Reid, R. Shine</i>	7.4 The recent de novo origin of protein C-termini <i>M. Andreatta, J. Levine, S. Foy, L. Guzman, M. Cordes, Joanna Masel</i>	3.15 dnaPipeTE, a new bioinformatic pipeline to assemble, annotate estimate abundance and dynamics of repetitive DNA in low coverage sequencing: application to <i>Aedes</i> mosquitoes <i>Clément Goubert, L. Modolo, C. Vieira, C. Valiente-Moro, P. Mavingui, M. Boulesteix</i>
17:30	6.5 Molecular-level response to selection in a mammalian laboratory model of a physiological and behavioral adaptation <i>Mateusz Konczal, W. Babik, J. Radwan, E. Sadowska, P. Koteja</i>	7.5 How novel proteins arise in evolution: the invention of protein structure and the flux of genes through genomes <i>Victor Luria, A. Karger, J. Cain, B. Olson, R. Neme, M. Kirschner</i>	3.16 The epigenetic interplay between transposable elements and their plant hosts <i>Alexandros Bousios, N. Darzentas, C. Diez, S. Takuno, B. Gaut</i>
17:45		Posters A	
18:30		Posters B	
19:15		Posters C	
20:00		Posters D	
20:45-21:00		Leave the building	

SMBE 2015, Hofburg Vienna, Austria

Late afternoon and Evening, Monday, July 13th

Time	Prinz Eugen	Ratstube	Notes
14:15		Poster Session: Posters A	
15:00		Poster Session: Posters B	
15:45-16:15		Coffee Break	
	8 The Horizontal Component of Microbial Evolution	5 Open Symposium	
16:15	8.1 CRISPR-cas systems as a barrier to lateral gene transfer in archaea - comparative genomics and experimental genetics <i>I. Turgeman, A. Naor, Y. Wolf, D. Christensen, E. Koonin, Uri Gophna</i>	5.11 Evolution at a single gene causes a difference in recombination rates between <i>Drosophila</i> species <i>Cara Brand, M. Cattani, S. Kingan, L. Wright, D. Presgraves</i>	
16:45	8.2 Parallel evolution of a global regulator ameliorates the cost of plasmid carriage <i>Ellie Harrison, S. Paterson, A. Spiers, M. Brockhurst</i>	5.12 The fossilised birth-death process applied to the total-evidence approach for dating with fossils <i>A. Gavryushkina, David Welch, T. Heath, A. Drummond, T. Stadler</i>	
17:00	8.3 Interactions between horizontally acquired genes create a fitness cost in <i>Pseudomonas aeruginosa</i> <i>Alvaro San Millan, M. Toll-Riera, Q. Qi, MacLean, MacLean</i>	5.13 The relationship between dN/dS and scaled selection coefficients: elucidating the properties, limitations, and capabilities of codon-based models <i>Stephanie Spielman, C. Wilke</i>	
17:15	8.4 Whole genome sequencing of non-vaccine pneumococcal serotypes from invasive disease reveals widespread but highly variable recombination <i>Cheryl Andam, P. Mitchell, A. Callendrello, L. McGee, L. Kim, B. Beall, M. Lipsitch, W. Hanage</i>	5.14 Heterogeneous characteristics of Conserved noncoding sequences in Eukaryotes <i>Nilmini Hettiarachchi, N. Saitou</i>	
17:30	8.5 Recombination drives the GC-content of bacterial genomes through biased gene conversion. <i>F. Iassalle, S. Pérían, T. Bataillon, X. Nesme, L. Duret, Vincent Daubin</i>	5.15 Deep sequencing of natural and laboratory populations of <i>Drosophila melanogaster</i> reveals new insights into the spectrum of de novo deleterious mutations <i>Zoe June Assaf, D. Petrov</i>	
17:45		Posters A	
18:30		Posters B	
19:15		Posters C	
20:00		Posters D	
20:45-21:00		Leave the building	

SMBE 2015, Hofburg Vienna, Austria

Early Morning, Tuesday, July 14th

Time	Festsaal	Zeremoniensaal	Forum
8:15-9:15	Plenary Talk: PI.3 Genomics of Rapid Adaptation <u><i>Dmitri Petrov</i></u>		
	6 Population Genomics of Rapid Adaptation (contin.)	7 Origins and evolution of molecular innovation (contin.)	9 Inference of demography and selection under violations of the Kingman coalescent assumptions
09:15	6.6 Predicting evolution using high resolution lineage tracking <u><i>Sasha Levy, J. Blundell, S. Venkataram, D. Petrov, D. Fisher, G. Sherlock</i></u>	7.6 Inter-kingdom horizontal gene transfer contributes to genomic innovations in diverse animal phyla <u><i>Sandie Degnan, S. Valverde, S. Higgie</i></u>	9.1 The effect of past demography and natural selection on the rate of evolution <u><i>Francois Balloux</i></u>
09:30		7.7 Evolutionary pervasive transcription across the genome is a continuous source of material for frequent de novo gene emergence. <u><i>Rafik Neme, D. Tautz</i></u>	
09:45	6.7 Extreme local adaptation in <i>Drosophila</i> chemosensory perception <u><i>J. Roman Arguello, M. Cardoso-Moreira, J. Mohammed, J. Grenier, S. Gottipati, A. Clark, R. Benton</i></u>	7.8 Elucidating the Sources of Species-Specific Genes <u><i>Bryan Moyers</i></u>	9.2 Estimating effective population size under inbreeding <u><i>B. Redelings, S. Kumagai, Marcy Uyenoyama</i></u>
10:00	6.8 Distinguishing modes of convergent adaptation in genomic data <u><i>Kristin Lee, G. Coop</i></u>	7.9 GenTree: an integrated resource for gene age dating and annotation refinement in human <u><i>Y. Shao, C. Chen, H. Shen, M. Long, Yong Zhang</i></u>	9.3 The seed-bank coalescent <u><i>Jochen Blath, B. Eldon, A. Casanova, N. Kurt, M. Berenguer</i></u>
10:15	6.9 Phenotypic adaptation due to recent environmental change <u><i>Susanne P. Pfeifer, S. Laurent, M. Foll, H. Hoekstra, E. Rosenblum, J. Jensen</i></u>	7.10 The place of De Novo Gene Origin in the Evolutionary Dynamics of the Genome-as-Population <u><i>Lee Altenberg</i></u>	9.4 Selection efficiency in chronic and acute malaria infections: The effect of overlapping generations <u><i>Hsiao-Han Chang, L. Childs, C. Buckee</i></u>
10:30	6.10 Adaptive convergence and quasi-heterozygous advantage after experimental evolution of <i>Escherichia coli</i> <u><i>Christian Sievert, T. Loeffler, L. Panyon, C. Morris, D. Winter, K. Dai, X. Wang, R. Cartwright</i></u>	7.11 Retrogenes illuminate dynamics of new gene structure and regulatory evolution in mammals <u><i>Francesco Nicola Carelli, M. Warnefors, H. Kaessmann</i></u>	9.5 Disentangling demography and selection effects in the cattle genome - new insights from the 1000 bull genomes project. <u><i>Simon Boitard, M. Dolezal, B. Servin, D. Fischer, J. Decker, I. MacLeod, Q. Zhang, B. Guldbbrandtsen, M. Lund, A. Bagnato, J. Vilkki, The 1000 bull genomes project</i></u>
10:45-11:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Early Morning, Tuesday, July 14th

Time	Prinz Eugen	Ratstube	Notes
8:15-9:15	Plenary Talk 3 (in Festsaal)		
	8 The Horizontal Component of Microbial Evolution (contin.)	5 Open Symposium	
09:15	8.6 Origins of major archaeal clades correspond to gene acquisitions from bacteria <i>Shijulal Nelson-Sathi, F. Sousa, M. Röttger, N. Lozada-Chávez, T. Thiergart, A. Janssen, D. Bryant, G. Landan, P. Schönheit, B. Siebers, J. McInerney, W. Martin</i>	5.16 An Approximate Bayesian Computation approach to reconstruct demography from sequence data. <i>Flora Jay, S. Boitard, F. Austerlitz</i>	
09:30	8.7 Evolutionary assembly patterns of prokaryotic genomes <i>Maximilian Press, C. Queitsch, E. Borenstein</i>		
09:45	8.8 Horizontal Transfer in <i>E.coli</i> plasmids. <i>Alice Ledda, C. Branger</i>	5.17 Physical and functional plastome reduction coincides with major shifts in substitution rates and relaxation of purifying selection in photosynthetic and nonphotosynthetic parasitic Orobanchaceae <i>Susann Wicke, K. Mueller, C. dePamphilis, G. Schneeweiss</i>	
10:00	8.9 Environmentally co-occurring mercury resistance plasmids have variable, context-dependent fitness effects and are phenotypically and genetically diverse <i>James Hall, E. Harrison, A. Lilley, S. Paterson, A. Spiers, M. Brockhurst</i>	5.2 Comparative analyses of four snake genomes provide important insights into trajectories of snake evolution <i>Qi Zhou, Z. Wang, W. Ying, G. Zhang, G. Yan</i>	
10:15	8.10 Molecular evolution of the pathogenicity and carbohydrate metabolism in mosquito-associated Spiroplasma <i>W. Lo, T. Chang, C. Ku, L. Chen, Chih-Horn Kuo</i>	5.19 Evolutionary and functional impact of polymorphic inversions in the human genome <i>Mario Cáceres, S. Villatoro, D. Castellano, M. Gayà-Vidal, C. Giner-Delgado, M. Oliva, D. Izquierdo, D. Vicente-Salvador, L. Pantano, M. Puig</i>	
10:30	8.11 Origin and spread of integron cassettes and how their fixation or loss shapes bacterial evolution <i>Jean Cury, T. Jové, E. Rocha</i>	5.20 Energy efficiency trade-offs drive nucleotide usage in transcribed regions <i>W. Chen, P. Bork, Martin Lercher</i>	
10:45-11:15		Coffee Break	

SMBE 2015, Hofburg Vienna, Austria

Late Morning, Tuesday, July 14th

Time	Festsaal	Zeremoniensaal	Forum
	10 Speciation genomics	11 PopGen in space! Theory and inference in spatial population genetics	12 Micro-evo-devo: using natural variation to explain the how and why of phenotypic evolution
		WILEY	WILEY
11:15	10.1 Speciation genomics: divergence continuum and beyond <i>Christian Lexer, M. Paris, D. Lindtke, C. Caseys, C. Christe, R. Wüest, E. Bossolini, M. Kessler, N. Salamin, K. Stölting</i>	11.1 Consequences of spatial expansions on population functional diversity <i>Laurent Excoffier, S. Peischl</i>	12.1 Micro-evolution of nematode vulval precursor cell fates <i>Marie-Anne Félix, M. Barkoulas, F. Besnard</i>
11:45	10.2 Rapid and complex genomic divergence during adaptive speciation in wild Solanum <i>Leonie Moyle, J. Pease, D. Haak, M. Hahn</i>	11.2 EEMS: a spatially explicit method to visualize geographic population structure and analyze non-stationary isolation by distance <i>Desislava Petkova, J. Novembre, M. Stephens</i>	12.2 Sexually dimorphic pigmentation in Drosophila: lineage sorting and independent comparisons in multiple phenotypic transitions <i>Sarah Signor, A. Kopp</i>
12:00	10.3 Heterogeneous genomic differentiation during repeated sympatric ecological speciation in Midas cichlid fishes <i>Axel Meyer, A. Kautt, G. Machado-Schiffiano</i>	11.3 The power of painting: using haplotype patterns to infer history <i>Garrett Hellenthal, L. Quinn, D. Lawson, D. Falush, S. Myers, S. Mead</i>	12.3 Gain and loss of GDF6 expression and the evolution of skeletal traits in fish and humans <i>Vahan Indjeian, D. Kingsley</i>
12:15	10.4 Genomics of Divergence along a Continuum Incipient Speciation <i>Philine Feulner</i>	11.4 New Routes to Phylogeography <i>Nicola De Maio, D. Wilson</i>	12.4 Natural variation at ath-miR824 modulates the adaptive potential of <i>Arabidopsis thaliana</i> <i>Jinyong Hu</i>
12:30	10.5 Speciation in cichlid fishes of Lake Malawi <i>Milan Malinsky, R. Challis, A. Tyers, E. Miska, M. Genner, R. Durbin, G. Turner</i>	11.5 Bayesian estimation of neighborhood size using composite marginal likelihoods <i>Tara Furstenu, R. Cartwright</i>	12.5 Size evolution in high-altitude Ethiopian <i>Drosophila melanogaster</i> : developmental decanalization and the genetics of a complex adaptive trait <i>Justin Lack, A. Yassin, D. Braun, M. Monette, J. Pool</i>
12:45-14:15	Lunch Break	13:00 – 14:00 NGS library construction: the frequently underestimated challenge NEBNext: Streamlined Library Prep Solutions	
14:15		Posters C	
15:00		Posters D	
15:45-16:15		Coffee Break	

SMBE 2015, Hofburg Vienna, Austria

Late Morning, Tuesday, July 14th

Time	Prinz Eugen	Ratstube	Notes
	13 Inferring fitness landscapes from experimental evolution	5 Open Symposium	
11:15	13.1 Inferring macroscopic epistasis from experimental evolution <i>Michael Desai</i>	5.21 Prevalence of episodic positive selection in immune genes of ants <i>Lumi Viljakainen, H. Havukainen, I. Salminen, S. Barribeau, Y. Wurm, H. Yan, S. Nygaard, M. Shiott, E. Privman</i>	
11:45	13.2 The adaptive fitness landscape in an experimentally evolving yeast population <i>Sandeep Venkataram, B. Dunn, Y. Li, K. Samerotte, L. Herissant, J. Chang, G. Sherlock, D. Petrov</i>	5.22 Local DNA topography predicts genomic mutation rates <i>Premal Shah, J. Plotkin</i>	
12:00	13.3 An intragenic fitness landscape spanned by beneficial mutations <i>Claudia Bank, R. Hietpas, S. Matuszewski, D. Bolon, J. Jensen</i>	5.23 Co-evolution of sexy proteins: characterizing the structural interactions of egg and sperm fertilization proteins by NMR <i>Damien Wilburn, W. Swanson</i>	
12:15	13.4 A Gaussian process model of genetic time series data arising in experimental evolution <i>Jonathan Terhorst, Y. Song</i>	5.24 Rethinking questions about evolution <i>David Penny</i>	
12:30	13.5 How good are statistical models at approximating high-dimensional fitness landscapes? <i>Louis du Plessis, G. Leventhal, S. Bonhoeffer</i>	5.25 Spore killer and its consequences on <i>Neurospora</i> populations <i>Ruxandra I. Molnar, H. Johannesson</i>	
12:45-14:15	Lunch Break		
14:15	Posters C		
15:00	Posters D		
15:45-16:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Afternoon, Tuesday, July 14th

Time	Festsaal	Zeremoniensaal	Forum
	10 Speciation genomics (contin.)	11 PopGen in space! Theory and inference in spatial population genetics (contin.) WILEY	14 Cancer as a Darwinian process
16:15	10.6 Deserts of diversity in the Human-Chimpanzee ancestor links the X chromosome to speciation. <i>Julien Dutheil, K. Munch, K. Nam, T. Mailund, M. Schierup</i>	11.6 Inferring dispersal from spatial patterns of IBD sharing <i>Harald Ringbauer</i>	14.1 Cancer, cooperation, and evolution <i>Natalia Komarova, D. Wodarz</i>
16:30	10.7 Disrupted imprinting, the large X-effect, and extreme hybrid overgrowth in hamsters <i>Thomas D Brekke, C. Callahan, J. Good</i>	11.7 Impact of Long-Range Dispersal on Range Expansions, Soft Sweeps and Genetic Hitchhiking <i>Oskar Hallatschek, D. Weissman</i>	
16:45	10.8 From sequences to molecular phenotypes: a simple model of transcription factor-DNA binding that predicts a higher rate of speciation in small populations. <i>Bhavin Khatri, R. Goldstein</i>	11.8 Evolution of quantitative traits under a migration-selection balance: when does skew matter? <i>Florence Debarre, S. Yeaman, F. Guillaume</i>	14.2 Sequencing and molecular evolutionary analysis of tumors within patients reveals that metastatic lineages can arise early and exhibit multiple genetic origins within primary tumors <i>Z. Zhao, B. Zhao, Y. Bai, A. Iamarino, S. Gaffney, J. Schlessinger, R. Lifton, D. Rimm, Jeffrey Townsend</i>
17:00	10.9 Reticulate speciation and adaptive introgression in the <i>Anopheles gambiae</i> species complex <i>Jacob E. Crawford, M. Riehle, W. Guelbeogo, A. Gneme, N. Sagnon, K. Vernick, R. Nielsen, B. Lazzaro</i>	11.9 Limits to a species' range in one- and two-dimensional habitats <i>Jitka Polechová, N. Barton</i>	14.3 Negative selection in the cancer genome <i>Donate Weghorn, S. Sunyaev</i>
17:15	10.10 Insights into speciation and introgression from 765 genomes of the main malaria vectors in Sub-Saharan Africa <i>Giordano Botta, A. Miles, B. Caputo, A. della Torre, D. Kwiatkowski, Anopheles gambiae 1000 Genomes Consortium</i>	11.10 Simulation of spatial processes shaping genetic diversity across time <i>Nuno M Silva, M. Currat</i>	14.4 Cancer across the tree of life: Cooperation and cheating in multicellularity <i>A. Aktipis, Amy Boddy, G. Jansen, U. Hibner, M. Hochberg, C. Maley, G. Wilkinson</i>
17:30	10.11 Same, same, but different: Quantitatively similar but qualitatively divergent paths to extremophile speciation in H ₂ S tolerant fish <i>Markus Pfenniger, S. Patel, M. Scharl, L. Arias-Rodriguez, M. Plath</i>	11.11 The effects of density-dependent range expansion on interspecific genetic introgression <i>Claudio S. Quilodrán, B. Nussberger, M. Currat, J. Montoya-Burgos</i>	14.5 Experimental evolution of motility in cancer cells <i>T. Taylor, A. Wass, P. Dash, Louise Johnson</i>
17:45-18:00	Leave the building		

SMBE 2015, Hofburg Vienna, Austria

Afternoon, Tuesday, July 14th

Time	Prinz Eugen	Ratstube	Notes
	13 Inferring fitness landscapes from experimental evolution (contin.)	15 The evolution of alternative splicing	
16:15	13.6 Discreteness and continuity in Adaptive Landscape <i>Olivier Tenaillon, H. Jacquier, A. Birgy, J. Guglielmini, A. Couce, H. Nagard</i>	15.1 Origins and impacts of new mammalian exons <i>J. Merkin, P. Chen, M. Alexis, S. Hautaniemi, Chris Burge</i>	
16:45	13.7 The effects of selection and mutation rate heterogeneity on parallel evolution in <i>Saccharomyces cerevisiae</i> <i>Susan Bailey, Q. Guo, F. Blanquart, T. Bataillon</i>	15.2 The importance of homology in alternative splicing <i>I. Ezkurdia, F. Abascal, J. Rodriguez, J. Rodriguez, E. Carillo, A. Pozo, J. Vazquez, A. Valencia, Michael Tress</i>	
17:00	13.8 Bacterial evolution of antibiotic hypersensitivity <i>Viktória Lázár, G. Singh, R. Spohn, I. Nagy, B. Papp, C. Pál</i>	15.3 The evolution of untranslated regions of mRNAs in primates <i>Iris Finci, A. Neacsulea, H. Kaessmann</i>	
17:15	13.9 Evolution of fitness trade-offs in locally adapted populations of <i>Pseudomonas fluorescens</i> <i>Alana Schick, S. Bailey, R. Kassen</i>	15.4 Appearance and fixation of alternative splicing events during evolution and their impact on the protein structures <i>Adel Ait-hamlat, L. Elodie, H. Richard</i>	
17:30	13.10 Fitness determines adaptability of highly diverse genotypes <i>Elizabeth Jerison, S. Kryazhimskiy, M. Desai</i>	15.5 Regulation of splicing factors by alternative splicing and NMD is conserved between kingdoms yet evolutionarily flexible <i>Liana Lareau, S. Brenner</i>	
17:45-18:00	Leave the building		

SMBE 2015, Hofburg Vienna, Austria

Early Morning, Wednesday, July 15th: Fitch Symposium

Time	Festsaal
08:15	Fitch Symposium
08:30	F.1 Inferring population structure across space and time <i>Gideon Bradburd, P. Ralph, G. Coop</i>
08:45	F.2 Watching the dynamics of molecular evolution over 60,000 generations <i>Benjamin Good, M. McDonald, R. Lenski, M. Desai</i>
09:00	F.3 Evolution of dosage compensation in the dioecious plant <i>Silene latifolia</i> <i>Aline Muyle, N. Zemp, C. Fruchard, A. Widmer, G. Marais</i>
09:15	F.4 Human epigenomic variation is driven by historical and recent changes in habitat and lifestyle <i>Fagny Maud, P. Etienne, M. Julia, R. Maxime, T. Flutre, M. Jones, Q. Hélène, H. Christine, M. Lisa, F. Alain, E. Heyer, A. Gessain, E. Betsem, P. Mouguiama-Daouda, J. Hombert, G. Perry, L. Barreiro, M. Kobor, L. Quintana-Murci</i>
09:30	F.5 Insights into recombination and sex chromosome evolution from whole-genome sequencing of platypus <i>Hilary Martin, E. Batty, J. Hussin, P. Westall, T. Daish, R. Bowden, T. Grant, F. Grutzner, J. Gongora, P. Donnelly</i>
09:45	F.6 Functional genetic analysis of stickleback craniofacial evolution <i>Priscilla Erickson, P. Cleves, J. Baek, C. Miller</i>
10:00	F.7 The dynamics of adaptive and antigenic evolution of influenza B virus <i>Pinky Langat, S. Watson, J. Raghwan, G. Dudas, C. Russell, R. Daniels, A. Rambaut, O. Pybus, J. McCauley, P. Kellam</i>
10:15	F.8 Epistasis Shaped the Evolutionary Sequence Space of an Ancestral Transcription Factor and its DNA Regulatory Elements <i>Alesia McKeown, D. Anderson, J. Thornton</i>
10:30-11:15	Coffee Break

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Continuation: next page

SMBE 2015, Hofburg Vienna, Austria

Late Morning, Wednesday, July 15th

Time	Festsaal	Zeremoniensaal	Forum
	16 Exploring the consequences of ancient and contemporary gene flow	11 PopGen in space! Theory and inference in spatial population genetics (contin.) WILEY	17 Genomics of sex bias: Addressing questions with or without genomes
11:15	16.1 Excavating archaic hominin DNA from the genomes of modern humans <u>Joshua Akey</u>	11.12 Insights into British and European population history from ancient DNA sequencing of Iron Age and Anglo-Saxon samples from East England. <u>Stephan Schiffels, W. Haak, B. Llamas, E. Popescu, L. Loe, R. Clarke, A. Lyons, P. Paajanen, D. Sayer, R. Mortimer, C. Tyler-Smith, A. Cooper, R. Durbin</u>	17.1 Recombination suppression in the sex chromosome system of the plant <i>Silene latifolia</i> <u>Deborah Charlesworth</u>
11:30		11.13 Genetic history of latin america: subcontinental ancestry and regional population structure <u>Juan Camilo Chacon-Duque, K. Adhikari, V. Acuna-Alonzo, S. Canizales-Quinteros, G. Bedoya, C. Gallo, G. Poletti, F. Rothhammer, M. Bortolini, R. Gonzalez-Jose, C. Consortium, G. Hellenthal, A. Ruiz-Linares</u>	
11:45	16.2 Introgressed Neandertal alleles contribute to gene expression differences among present-day humans. <u>Michael Dannemann, A. Andrés, J. Kelso, P. Khaitovich, E. Khrameeva, K. Prüfer</u>	11.14 Exploring population separation history using physically phased genomes <u>Shiya Song, E. Sliwerska, S. Emery, J. Kidd</u>	17.2 Comparative analysis of X chromosome gene regulation in nematodes <u>S. Albritton, M. Kramer, A. Kranz, <u>Sevinc Ercan</u></u>
12:00	16.3 Comprehensive phenome-wide association analysis of Neanderthal introgression supports its relevance to disease risk in modern humans <u>Corinne Simonti, B. Vernot, J. Denny, J. Akey, J. Capra</u>	11.15 Inferring selection from a spatially explicit demographic model based on a large number of human populations. <u>Benjamin Peter, J. Novembre</u>	17.3 Numerous transitions of sex chromosomes in Diptera <u>Beatriz Vicoso, D. Bachtrög</u>
12:15	16.4 Genetic consequences of hybridization of diverged stocks of endangered Australian freshwater fish after translocations early in the 20th century <u>Alexandra Pavlova, S. Amish, L. Beheregaray, R. Coleman, D. Gilligan, B. Ingram, J. Kearns, A. Lamb, M. Lintermans, G. Luikart, J. Lyon, S. Narum, M. Sasaki, Z. Tonkin, P. Sunnucks</u>	11.16 Evidence for a common origin of Blacksmiths and Cultivators in the Ethiopian Ari within the last 4500 years: Lessons for clustering-based inference <u>Lucy van Dorp, D. Balding, S. Myers, L. Pagani, C. Tyler-Smith, E. Bekele, A. Tarekegn, M. Thomas, N. Bradman, G. Hellenthal</u>	17.4 A novel fine-scale human recombination map reveals sex differences <u>Chenling Xu, G. Coop</u>
12:30	16.5 The roles of shared ancestry and shared genes in niche adaptation in <i>Aeromonas</i> <u>Johann Peter Gogarten, M. Fullmer, S. Colston, J. Graf</u>	11.17 The evolutionary genomics of a recent invasion: a natural mutation accumulation line of North American <i>Arabidopsis</i> depicted using historic herbarium samples <u>Moises Exposito-Alonso, C. Becker, D. Weigel, H. Burbano</u>	17.5 Multifactorial Male Determination in the House Fly Primarily affects the Expression of Male-Biased Genes <u>Richard Meisel, J. Scott, A. Clark</u>
12:45-14:15	Lunch Break with Posters	13:00 – 14:00 NGS library construction: the frequently underestimated challenge Fasteris: Insights from a professional service provider	

SMBE 2015, Hofburg Vienna, Austria

Late Morning, Wednesday, July 15th

Time	Prinz Eugen	Ratstube	Notes
	18 Within- and between-host viral evolution	19 Novel Functional Approaches to Evolutionary Genomics	
11:15	18.1 Using viral genetic data to study evolution and replication during chronic viral infection <i>Oliver Pybus</i>	19.1 Developmental mechanisms underlying differences in cerebral cortex size in humans and other primates <i>Rick Livesey</i>	
11:45	18.2 Plant and algal genomes enclose footprints of past infections by giant virus relatives <i>Guillaume Blanc, L. Gallot, A. Epert, F. Nogu�, F. Maumus</i>	19.2 Primate iPSCs provide a window into the evolution of key metabolic traits <i>Gregory Wray, S. Makohon-Moore</i>	
12:00	18.3 Population genetics of Ebola virus in West Africa <i>Gytis Dudas, A. Rambaut</i>	19.3 Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species <i>Charles Danko, A. Martins, H. Yang, J. Lis, L. Kraus, A. Siepel</i>	
12:15	18.4 Population genomics of within host HIV evolution <i>F. Zanini, J. Albert, Richard Neher</i>	19.4 Outbred genome sequencing and CRISPR/Cas9 gene editing in butterflies <i>Xueyan Li, D. Fan, W. Zhang, G. Liu, L. Zhang, L. Zhao, X. Fang, L. Chen, J. Wang, G. Zhang, M. Kronforst, W. Wang</i>	
12:30	18.5 A fighter after all: Accessory protein of minor HIV group under positive selection in arms race with human innate immunity factor <i>Christopher Monit, R. Goldstein</i>	19.5 Novel functional approaches to study regulatory evolution in cichlid fishes. <i>Claudius F Kratochwil, A. Meyer</i>	
12:45-14:15	Lunch Break with Posters		

SMBE 2015, Hofburg Vienna, Austria

Early Afternoon, Wednesday, July 15th

Time	Festsaal	Zeremoniensaal	Forum
	16 Exploring the consequences of ancient and contemporary gene flow (contin.)	20 Evolution of molecular pathways and networks: Molecular evolution meets systems biology	17 Genomics of sex bias: Addressing questions with or without genomes (contin.)
14:15	16.6 Probabilities and patterns of adaptive introgression <i>Joachim Hermissson, D. Setter, H. Uecker, J. Jensen</i>	20.1 The evolution of heritable human disease: what's a disease gene? <i>David Robertson</i>	17.6 Evolution and turnover of vertebrate sex chromosomes <i>Jennifer A. Marshall Graves</i>
14:45	16.7 Detecting adaptive introgression in humans <i>Emilia Huerta-Sanchez, F. Racimo, R. Nielsen</i>	20.2 An adaptive scenario for the origins of complex innovations <i>Balázs Papp, B. Szappanos, C. Pál, B. Csörgő, V. Lázár, G. Fekete, R. Notebaart, X. Lu, C. Fritzemeier, M. Lercher</i>	17.7 Genetic basis of genital evolution between <i>Drosophila</i> species <i>K. Tanaka, C. Hopfen, M. Herbert, C. Schlötterer, D. Stern, J. Masly, A. McGregor, Maria Daniela Santos Nunes</i>
15:00	16.8 Evaluating genomewide introgression in <i>Drosophila yakuba</i> and <i>D. santomea</i> <i>Ana Llopart</i>	20.3 Phenotypic and molecular evolution of the bacterial chemotaxis network <i>A. Gonzalez, Sander van Doorn</i>	17.8 Variable autosomal and X divergence estimates near and far from genes in great apes <i>Pooja Narang, M. Sayres</i>
15:15	16.9 450 diverse high coverage whole genome sequences reveal ancient population admixture in modern human populations <i>Luca Pagani</i>	20.4 Modeling Duplicate Genes in Populations, in Genomes, and in Complexes <i>A. Teufel, A. Konrad, J. Masel, L. Liu, David Libertes</i>	17.9 Modeling population size changes leads to accurate inference of sex-biased demographic events <i>Shaila Musharoff, S. Shringarpure, C. Bustamante, S. Ramachandran</i>
15:30	16.10 Genomic signatures and mechanisms of introgression between domestic and wild animals: the case of a gene important for immunity <i>Christine Grossen, H. Lischer, D. Croll, L. Keller</i>	20.5 Turnover of phosphorylation sites in disordered regions: exploring a stabilizing selection hypothesis <i>Taraneh Zarin, A. Moses</i>	17.10 Sex-biased expression and evolutionary rates in brown algae (Phaeophyceae; Heterokontophyta): the importance of genes uniquely expressed in males <i>Gareth Pearson, B. Liu, J. Coimbra, A. Anjos, E. Serrão</i>
15:45-16:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Early Afternoon, Wednesday, July 15th

Time	Prinz Eugen	Ratstube	Notes
	18 Within- and between-host viral evolution (contin.)	21 Fungal Evolutionary Genomics: Unravelling Mysteries from the Forgotten Kingdom	
14:15	18.6 The effects of a deleterious mutation load on patterns of influenza's antigenic evolution in humans <i>K. Koelle, David Rasmussen</i>	21.1 Evolutionary genomics of early branches of the fungal tree <i>Jason Stajich, G. Benny, M. Berbee, N. Corradi, I. Grigoriev, A. Gryganskyi, T. James, A. Kuo, K. O'Donnell, R. Roberson, M. Smith, J. Spatafora, T. Taylor, R. Vilgalys, M. White</i>	
14:45	18.7 Less efficient drugs lead to softer sweeps in intra-patient populations of HIV-1 <i>Alison Feder, S. Rhee, R. Shafer, D. Petrov, P. Pennings</i>	21.2 History of Lachancea genomes inferred from extant species sequencing and extinct ancestor reconstructions <i>V. Sarilar, G. Drillon, N. Vakirlis, I. Lafontaine, J. Meyniel, C. Neuvéglise, Gilles Fischer</i>	
15:00	18.8 Extreme heterogeneity in genetic diversity and molecular evolution found in chronic HCV infection <i>Jayna Raghwanj, R. Rose, I. Sheridan, P. Lemey, M. Suchard, P. Farci, P. Klenerman, O. Pybus</i>	21.3 iGénolevures, a new consortium for yeast comparative genomics <i>C. Fairhead, Cécile Neuvéglise, iGénolevures consortium</i>	
15:15	18.9 Genome-wide recombination is a major driver of human cytomegalovirus evolution <i>Florent Lassalle, D. Depledge, M. Reeves, A. Brown, M. Christiansen, H. Tutill, R. Williams, K. Einer-Jensen, J. Holdstock, C. Atkinson, J. Brown, F. Loenen, D. Clark, P. Griffiths, G. Verjans, M. Schutten, R. Milne, F. Balloux, J. Breuer</i>	21.4 Long-read sequencing of Spore killer strains of Neurospora reveals highly divergent genomic architectures and a complex evolutionary history <i>Jesper Svedberg, T. Hammond, H. Johannesson</i>	
15:30	18.10 Host-driven mutation drives genome evolution of sigma virus (DMelSV; Rhabdoviridae) in <i>Drosophila melanogaster</i> <i>Marta Wayne, H. Piontkivska, L. Matos, M. Miyamoto</i>	21.5 Adaptive genome remodelling by horizontal transfers in cheese-making fungi <i>Ricardo Rodríguez de la Vega, J. Ropars, M. Lopez-Villavicencio, J. Gouzy, E. Sallet, E. Dumas, S. Lacoste, R. Debuchy, A. Branca, T. Giraud</i>	
15:45-16:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Late Afternoon, Wednesday, July 15th

Time	Festsaal	Zeremoniensaal	Forum
	<p>22 Adaptive and non-adaptive evolution of gene expression and regulation</p> <p></p>	<p>20 Evolution of molecular pathways and networks: Molecular evolution meets systems biology (contin.)</p>	<p>23 Reframing the demography vs. selection debate using 21st century models and data</p>
16:15	<p>22.1 Differential adaptation to lakes and rivers: insights from transcriptome analyses in sticklebacks <i>Yun Huang, P. Feulner, F. Chain, M. Panchal, C. Eizaguirre, T. Lenz, I. Samonte, M. Kalbe, M. Stoll, E. Bornberg-Bauer, Th Reusch, M. Milinski</i></p>	<p>20.6 Inferences of selection in protein networks from genomic data and detailed network- and population-scale models <i>Ryan Gutenkunst</i></p>	<p>23.1 The history of migrations and adaptations to high altitude in humans <i>Anna Di Rienzo, C. Jeong, B. Basnyat, G. Childs, S. Craig, M. Neupane, J. Marcus, D. Witonsky, J. Novembre, C. Beall</i></p>
16:30	<p>22.2 The navigability of more than 1000 empirical adaptive landscapes of transcription regulation <i>José Aguilar-Rodríguez, J. Payne, A. Wagner</i></p>		
16:45	<p>22.3 Dynamics of Transcription Factor Binding Site Evolution <i>Murat Tugrul, T. Paixao, G. Tkacik, N. Barton</i></p>	<p>20.7 The protein-protein network hub, Hsp90, does not provide robustness to new mutations in yeast <i>Kerry Geiler-Samerotte, Y. Zhu, D. Hall, M. Siegal</i></p>	<p>23.2 Robust inference of selection against maladaptive gene flow <i>Simon Aeschbacher, G. Coop</i></p>
17:00	<p>22.4 Conserved microRNA editing in mammalian evolution, development and disease <i>Maria Warnefors, A. Liechti, J. Halbert, D. Valloton, H. Kaessmann</i></p>	<p>20.8 Genomic landscape of compensatory evolution <i>Csaba Pal</i></p>	<p>23.3 Robust estimation of the distribution of fitness effects (DFE) of new mutations from genome-wide patterns of polymorphism and divergence <i>Paula Tataru, M. Mollion, M. Franco, N. Galtier, S. Glemin, T. Bataillon</i></p>
17:15	<p>22.5 Evolution of microRNA across primates <i>Jennifer McCreight, W. Swanson</i></p>	<p>20.9 Molecular evolution informs systems biology: inference of global gene networks through correlated evolution <i>R. Partha, Z. Ferreira, N. Priedigkeit, A. O'Donnell, Nathan Clark</i></p>	<p>23.4 Selection and demography in triallelic sites: a diffusion approach and application to nonsynonymous sites <i>Aaron Ragsdale, R. Gutenkunst</i></p>
17:30	<p>22.6 The target repertoire of each miRNA increases during evolution <i>Masafumi Nozawa</i></p>	<p>20.10 Coevolution of Rubisco and its chaperones <i>Maxim Kapralov</i></p>	<p>23.5 Inferring the recent evolutionary history of the sibling species pair, <i>Solanum peruvianum</i> and <i>S. chilense</i>, using 21st century models and data. <i>Laura Rose, A. Reddy, P. Staab, D. Metzler</i></p>
17:45-18:00	Leave the building		

SMBE 2015, Hofburg Vienna, Austria

Late Afternoon, Wednesday, July 15th

Time	Prinz Eugen	Ratstube	Notes
	24 Short Tandem Repeats in the Post-Genomics Age: Accurate Typing, Variability, Evolution, and Function	21 Fungal Evolutionary Genomics: Unravelling Mysteries from the Forgotten Kingdom (contin.)	
16:15	24.1 Genome-Wide Analysis of Expression Short Tandem Repeats in Human <i>M. Gymrek, T. Willems, B. Markus, S. Georgiev, J. Pritchard, <u>Yaniv Erlich</u></i>	21.6 Population genomics of a highly diverse sexual pathogen: the origin and fate of chromosomal structural variants in populations <i>Daniel Croll, F. Hartmann, M. Zala</i>	
16:30		21.7 A new intracellular parasite is a missing link between fungi and microsporidia <i>Karen Haag, D. Ebert, T. James, J. Pombert, R. Larsson</i>	
16:45	24.2 A first survey of tandem repeat instabilities and associated gene expression changes in 35 colorectal cancers <i>Tugce Bilgin Sonay, M. Koletou, A. Wagner</i>	21.8 Transposable elements promote adaptive evolution in the genome of the fungal wheat pathogen <i>Zymoseptoria tritici</i> <i>Jonathan Grandaubert, J. Dutheil, E. Stukenbrock</i>	
17:00	24.3 The evolution of short indels at meiotic recombination hotspots <i>Angelika Heißl, B. Arbeithuber, I. Tiemann-Boege</i>	21.9 Evolutionary analysis and manipulation of natural <i>Saccharomyces</i> genomes <i>Chris Todd Hittinger, Q. Langdon, D. Peris, W. Alexander, R. Moriarty, K. Sylvester, D. Libkind, P. Goncalves, J. Sampaio</i>	
17:15	24.4 Accurate typing of Short Tandem Repeats from genome-wide sequencing data and its applications <i>A. Fungtammasan, G. Ananda, S. Hile, M. Su, C. Sun, R. Harris, P. Medvedev, K. Eckert, <u>Kateryna Makova</u></i>	21.10 Experimental evolution with transgenic <i>Saccharomyces cerevisiae</i> strains illustrates massive amplifications of chromosomal segments forming macrotene chromosomes <i>Bernard Dujon, Varun, Khanna, Agnès Thierry</i>	
17:30	24.5 Microsatellite tandem repeats are abundant in mammalian and avian promoters and are associated with regulatory elements <i>Neil Gemmell, H. Abe, S. Sawaya</i>	21.11 Insights into the origin and evolution of yeast mating-type switching mechanisms from a chromosomal inversion system in methylotrophs <i>Sara J. Hanson, K. Byrne, K. Wolfe</i>	
17:45-18:00	Leave the building		

SMBE 2015, Hofburg Vienna, Austria

Early Morning, Thursday, July 16th

Time	Festsaal	Zeremoniensaal	Forum
	22 Adaptive and non-adaptive evolution of gene expression and regulation (contin.) LEXOGEN	4 Origins and evolution of molecular innovation (contin.)	23 Reframing the demography vs. selection debate using 21st century models and data (contin.)
08:15	22.7 Genome-wide inference of natural selection on regulatory sequences in the human genome <u>Adam Siepel</u>	4.11 Conformational strain in newly evolved protein folds <i>V. Kumirov, E. Dykstra, T. Szyszka, Matthew Cordes</i>	23.6 Expansion Out of Africa Affected Accumulation of Deleterious Alleles in Diverse Human Genomes <u>Brenna Henn</u>
08:30		4.12 Evolutionary connections and constraints between enzymes in the MBL superfamily <i>Nobuhiko Tokuriki</i>	
08:45	22.8 Polygenic Adaptation in Recent Human History <u>Yair Field, J. Pritchard</u>	4.13 Combinatorial DNA rearrangement facilitates the origin of new genes in ciliates <i>X. Chen, Laura Landweber</i>	23.7 The dark side of domestication: Deleterious variation in the dog genome <i>C. Marsden, D. Vecchyo, G. Johnson, R. Schnabel, R. Wayne, Kirk Lohmueller</i>
09:00	22.9 Functional characterization of an adaptive cis-regulatory polymorphism in <i>Drosophila melanogaster</i> <i>A. Glaser-Schmitt, John Parsch</i>	4.14 Mistranslation drives the evolution of robustness in experimental populations of TEM-1 β -lactamase <i>Sinisa Bratulic, F. Gerber, A. Wagner</i>	23.8 Shifts in selective pressure or random genetic drift? From balancing to positive selection out of Africa <i>Cesare de Filippo, F. Key, S. Ghirotto, A. Benazzo, P. Kleinert, J. Meneu, A. Weihmann, N. Program, G. Parra, E. Green, A. Andrés</i>
09:15	22.10 Towards an understanding of the genetic basis of phenotypic change - changes in the expression of a microRNA underlie morphological change in <i>Drosophila melanogaster</i> <u>Sebastian Kittelmann, S. Arif, I. Almudi, M. Nunes, A. McGregor</u>	4.15 The genomic architecture of metabolic evolutionary innovation in <i>Pseudomonas aeruginosa</i> <i>Macarena Toll-Riera, A. Millan, A. Wagner, C. MacLean</i>	23.9 Measurement of selection in humans by the analysis of autozygous regions in 3,222 exome sequences from a highly endogamous population <i>Vagheesh Narasimhan, K. Karczewski, H. Karen, Y. Xue, P. Danecek, S. McCarthy, T. Chris, C. Griffiths, D. Mason, J. Wright, E. Maher, D. MacArthur, T. Richard, D. Heel, D. Richard</i>
09:30	22.11 Characterizing adaptively introgressed Neanderthal haplotypes in modern humans <u>Rachel Gittelman, B. Vernot, J. Akey</u>	4.16 Forecasting Evolutionary Adaptation by Mapping the Innovative Potential of Underground Metabolism <i>Balint Kintses, R. Notebart, B. Szappanos, F. Pal, A. Gyorkey, B. Bogos, V. Lazar, R. Spohn, B. Csorgo, C. Pal, B. Papp</i>	23.10 Pervasive long-range linkage disequilibrium in <i>D. melanogaster</i> <u>Nandita Garud, D. Petrov</u>
09:45	22.12 Adaptive and non-adaptive effects of a <i>Drosophila melanogaster</i> natural mutation through different molecular mechanisms <i>L. Guio, Josefa Gonzalez</i>	4.17 The evolutionary potential of cis-regulatory mutations for sudden changes in development <u>Paulo Pinto</u>	23.11 Determinants of adaptive evolution in great apes <i>K. Nam, T. Mailund, G. Project, K. Munch, Mikkel Heide Schierup</i>
10:00	22.13 Expression Piggy-backing: Neighboring genes show correlated evolution in gene expression <u>Avazeh Ghanbarian, L. Hurst</u>	4.18 Evolution of gene expression associated with innovation and evolution of feathers <i>Jacob Musser, C. Liang, G. Wagner, R. Prum</i>	23.12 Background Selection Drives Population Specific Patterns of Diversity and Biases Demographic Inference in Humans <u>Raul Torres, R. Hernandez</u>
10:15	22.14 Role of transcriptomic plasticity in adaptation to new environments <u>Saad Arif, L. Tan, D. Kingsley, F. Jones</u>	4.19 Experimental evolution of increased efficiency through serial propagation in emulsion <i>Iraes Rabbers, H. Bachmann, B. Teusink</i>	23.13 Novel probabilistically interpretable methods for localizing targets of selective sweeps <i>L. Sugden, Sohini Ramachandran</i>
10:30	22.15 DNA methylation variation in Arabidopsis has a genetic basis and shows evidence of local adaptation <u>Manu Dubin, P. Zang, D. Meng, M. Remigereau, E. Osborne, F. Casale, P. Drew, G. Jean, A. Kahles, B. Vilhjálmsson, J. Jagoda, S. Irez, V. Vornin, Q. Song, Q. Long, G. Rättsch, O. Stegele, R. Clark, M. Nordborg</u>	4.20 Origins of developmental enhancer functions in the neocortex <u>Deena Emera, J. Yin, S. Reilly, J. Noonan</u>	23.14 Habitat shift model supports demography as the main driver of genome evolution <u>Tristan Lefebure, C. Morvan, F. Malard, L. Konecny-Dupre, L. Gueguen, M. Weiss-Gayet, A. Seguin-Orlando, L. Ermini, C. Sarkissian, P. Charrier, D. Eme, C. Francois, L. Duret, C. Vieira, L. Orlando, C. Douady</u>
10:45-11:15	Coffee Break		


SMBE 2015, Hofburg Vienna, Austria

Early Morning, Thursday, July 16th

Time	Prinz Eugen	Ratstube	Notes
	25 Ancient Genomes: A Time Machine for Investigating Natural Selection	26 Genomic and Epigenomic Evolution of Sex Chromosomes: Broad Patterns and Intriguing Cases	
08:15	25.1 Ancient <i>Mycobacterium tuberculosis</i> genomes suggest re-adaption to pre-Columbian human populations <i>Johannes Krause, K. Bos, A. Herbig, S. Gagneux, J. Buikstra, A. Stone</i>	26.1 Genomic evolution of two Y chromosomes in papaya <i>Ray Ming</i>	
08:45	25.2 A paleogenomic perspective on horse domestication. <i>Ludovic Orlando</i>	26.2 Faster-X effects and gene expression bias in <i>Drosophila melanogaster</i> <i>Brian Charlesworth, V. Avila, J. Campos</i>	
09:00		26.3 Genetic and epigenetic mechanisms to trigger off sexual dimorphism, Example of intriguing dioecious Schistosomatidae parasite. <i>M. Picard, C. Grunau, D. Roquis, J. Allienne, D. Duval, J. Boissier, Céline Cosseau</i>	
09:15	25.3 Ancient genomes improve our understanding of modern human population differentiation <i>Felix M. Key, Q. Fu, F. Romagné, M. Lachmann, A. Andrés</i>	26.4 Unprecedented support for Ohno's hypothesis of dosage compensation from an ancient reptilian sex chromosome system <i>Ray Marin, D. Cortez, S. Mahadevaiah, P. Julien, A. Liechti, J. Halbert, D. Valloton, K. Ascencao, H. Kerver, J. Wade, P. Tschopp, J. Turner, H. Kaessmann</i>	
09:30	25.4 Quantifying selection against Neanderthal introgression <i>Ivan Juric, G. Coop, S. Aeschbacher</i>	26.5 Sexual selection drives short- and long-term evolution of the avian Z chromosome <i>Alison Wright, P. Harrison, F. Zimmer, S. Montgomery, M. Pointer, J. Mank</i>	
09:45	25.5 Ancient Exomes of Individuals from the Pacific Northwest Coast Reveal Immune-Based Adaptations to the Americas <i>John Lindo, M. DeGiorgio, R. Malhi</i>	26.6 A recent bottleneck of Y chromosome diversity coincides with a global change in culture <i>Toomas Kivisild</i>	
10:00	25.6 Disentangling natural selection from drift using forward simulations based on ancient genetic data <i>Karola Kirsanow, A. Powell, M. Thomas, J. Burger</i>	26.7 Diversity varies across recombining and non-recombining regions of the human sex chromosomes <i>Melissa Wilson Sayres</i>	
10:15	25.7 Testing directional selection on polygenic traits using ancient DNA <i>John Novembre, C. Chiang, J. Marcus</i>	26.8 Comparative Analysis of the Y Chromosome Genomes from Greater Apes <i>Monika Michalovova, M. Tomaszewicz, S. Rangavittal, R. Sanchez, H. Fescemyer, O. Ryder, M. Ferguson-Smith, R. Chikhi, P. Medvedev, K. Makova</i>	
10:30	25.8 Detecting ancient selective sweeps in modern humans using the genomes of our closest extinct relatives <i>Stéphane Peyrégne, C. Theunert, M. Dannemann, M. Lachmann, M. Stoneking, K. Prüfer</i>	26.9 Wolbachia bacterial endosymbionts and the evolution of sex determination in the isopod <i>Armadillidium vulgare</i> <i>S. Leclercq, J. Thézè, I. Giraud, A. Chebbi, B. Moumen, L. Ernenwein, P. Grève, C. Gilbert, Richard Cordaux</i>	
10:45-11:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Late Morning, Thursday, July 16th

Time	Festsaal	Zeremoniensaal	Forum
	<p>22 Adaptive and non-adaptive evolution of gene expression and regulation (contin.)</p> <p></p>	10 Speciation genomics (contin.)	1 Beyond the Equilibrium Paradigm: The role of temporal processes in population genetics and evolution (contin.)
11:15	<p>22.16 Alternative splicing: widespread fine-tuning regulatory process or costly errors? A. Popa, B. Saudemont, J. Parmley, O. Arnaiz, L. Sperling, E. Meyer, <u>Laurent Duret</u></p>	<p>10.12 Genetics and molecular mechanisms affecting polyploidy-dependent speciation <u>Luca Comai</u>, I. Henry</p>	1.12 Using time-resolved genetic data to monitor evolving populations <u>Ville Mustonen</u>
11:45	<p>22.17 Fixation of gene duplications due to beneficial increases in gene expression <u>Margarida Cardoso-Moreira</u>, J. Arguello, D. Riccardi, S. Gottipati, L. Harshman, J. Grenier, A. Clark</p>	<p>10.13 Recent allopolyploid origins and the early stages of diploidization in the highly successful tetraploid <i>Capsella bursa-pastoris</i> <u>Kim A. Steige</u>, G. Douglas, G. Gos, A. Salcedo, K. Holm, E. Josephs, R. Arunkumar, J. Ågren, K. Hazzouri, W. Wang, A. Platts, R. Williamson, B. Neuffer, D. Scofield, M. Lascoux, S. Wright, T. Slotte</p>	1.13 A model of protein evolution within fitness landscape changing with time <u>Dinara Usmanova</u> , I. Povolotskaya, F. Kondrashov
12:00	<p>22.18 Long-term survival of duplicate genes despite absence of subfunctionalized expression. <u>Xun Lan</u>, J. Pritchard</p>	<p>10.14 Allopolyploidy-associated changes of genome composition in genus <i>Melampodium</i>: does evolution repeat itself? <u>Jamie McCann</u>, J. Macas, P. Novák, T. Stuessy, J. Villaseñor, H. Weiss-Schneeweiss</p>	1.14 The fate of a mutation in a fluctuating environment <u>Ivana Cvijovic</u> , B. Good, M. Desai
12:15	<p>22.19 Duplication and functional divergence of miRNAs in the spider <i>Parasteatoda tepidariorum</i> D. Leite, M. Ninova, E. Schwager, M. Hilbrant, A. Buffry, S. Griffiths-Jones, M. Ronshaugen, <u>Alistair P. McGregor</u></p>	<p>10.15 The Effects of Pollination and Range Shifts on the Diversification of the Tribe Antirrhineae <u>Ezgi Ogutcen</u>, J. Theriault, D. King, J. Vamosi</p>	1.15 Fluctuations in traveling wave models of asexual adaptation: large scale oscillations in fitness variance <u>Lukas Geyrhofer</u> , O. Hallatschek
12:30	<p>22.20 Evolutionary changes in target genes of ZEB2, a transcription factor involved in brain development and mental retardation S. Berto, A. Erpf, L. Falkowski, K. Jacob, <u>Katja Nowick</u></p>	<p>10.16 Pollinator-mediated divergent selection drives reproductive isolation, speciation, and the evolution of barrier genes in sexually deceptive orchids <u>Philipp Schlüter</u>, K. Sedeek, E. Whittle, J. Shanklin</p>	1.16 The Evolutionarily Stable Distribution of Fitness Effects <u>Daniel P. Rice</u> , B. Good, M. Desai
12:45-14:15	Lunch Break (Take down posters at the end)		

SMBE 2015, Hofburg Vienna, Austria

Late Morning, Thursday, July 16th

Time	Prinz Eugen	Ratstube	Notes
	2 Untangling information, noise, and phylogenetic reconstruction in genome scale data (contin.)	27 The origins of multicellularity under the light of functional genomics	
11:15	2.11 Rapid identification of phylogenetically informative data from next-gen sequencing reads <i>Rachel Schwartz, R. Cartwright</i>	27.1 <i>S. rosetta</i> as a simple model for animal multicellularity <i>Nicole King</i>	
11:30	2.12 Bayesian information content estimation and application to phylogenomics <i>Karolina Fucikova, P. Lewis, M. Chen, L. Kuo, L. Lewis</i>		
11:45	2.13 Parametric estimation of evolutionary constraint using amino acid sequences <i>Daniel Jordan, I. Adzhubey, S. Sunyaev</i>	27.2 Peering into the pond for clues to multicellularity <i>Bradley J. S. C. Olson</i>	
12:00	2.14 Using three-dimensional structure in inferring deep homology <i>Toni Daly, A. Sutherland-Smith, D. Penny</i>	27.3 Insights into evolution of eumetazoan regulatory developmental networks from the sea anemone <i>Nematostella vectensis</i> <i>Ulrich Technau</i>	
12:15	2.15 How Evolution of Genomes Is Reflected In Exact DNA Sequence Match Statistics <i>Florian Massip, M. Sheinman, S. Schbath, A. Peter</i>	27.4 Origin of animal transcriptional regulation: insights from a sponge with both unicellular and multicellular genomic characteristics <i>S. Fernandez-Valverde, Bernard Degnan</i>	
12:30	2.16 Statistical Properties of Pairwise Distances between Leaves on a Random Yule Tree <i>Michael Sheinman, F. Massip, P. Arndt</i>	27.5 Functional evolution of a bacterial small RNA that controls multicellular fruiting body development <i>I-Chen Kimberly Chen, G. Velicer, Y. Yu</i>	
12:45-14:15		Lunch Break (Take down posters at the end)	

SMBE 2015, Hofburg Vienna, Austria

Early Afternoon, Thursday, July 16th

Time	Festsaal	Zeremoniensaal	Forum
	<p>22 Adaptive and non-adaptive evolution of gene expression and regulation (contin.)</p> <p>LEXOGEN</p>	<p>6 Population Genomics of Rapid Adaptation (contin.)</p>	<p>11 PopGen in space! Theory and inference in spatial population genetics (contin.)</p> <p>WILEY</p>
14:15	<p>22.21 Evolution of toxin resistance via polygenic cis-regulatory adaptation <i>S. Naranjo, J. Smith, C. Artieri, M. Zhang, Y. Zhou, M. Palmer, Hunter Fraser</i></p>	<p>6.11 Within-host adaptation of Mycobacterium tuberculosis <i>M. O'Neill, T. Mortimer, <u>Caitlin Pepperell</u></i></p>	<p>11.18 Identifying selected loci in a flower colour hybrid zone <i>Nick Barton, D. Field, H. Tavares, E. Coen</i></p>
14:30	<p>22.22 Disentangling the effects of mutation and selection on the evolution of gene expression <i>Brian Metzger, D. Yuan, F. Duveau, P. Wittkopp</i></p>	<p>6.12 The impact of gene flow, standing genetic variations and strong artificial selection during pig domestication <i>Laurent Frantz, J. Schraiber, V. Battista, M. Groenen, G. Larson</i></p>	
14:45	<p>22.23 Stabilizing selection and lineage specific evolution of stress response in <i>Saccharomyces sensu stricto</i> <i>Joshua Schraiber, S. Kim, J. Madeoy, J. Akey</i></p>	<p>6.13 The role of recombination in evolutionary rescue <i>Hildegard Uecker, J. Hermisson</i></p>	<p>11.19 Ancient divergence and repeated adaptive radiation in Macaronesian Islands Arabidopsis <i>Andrea Fulgione, X. Pico, C. Alonso-Blanco, J. Hermisson, A. Hancock</i></p>
15:00	<p>22.24 Variation of gene expression response to developmental temperature of two natural populations affects their evolutionary response in novel thermal environment. <i>François Mallard, R. Tobler, V. Nolte, C. Schlötterer</i></p>	<p>6.14 The genomic signature of stabilizing selection during temperature adaptation in experimental <i>Drosophila melanogaster</i> populations <i>Susanne Franssen, R. Kofler, V. Nolte, C. Schlötterer</i></p>	<p>11.20 Molecular evolutionary consequences of island colonisation <i>Jennifer James, R. Lanfear, A. Eyre-Walker</i></p>
15:15	<p>22.25 Analysis of allele-specific expression in F1 hybrids reveals cis-regulatory changes associated with recent adaptive floral evolution in <i>Capsella rubella</i> <i>K. Steige, J. Reimegård, D. Koenig, D. Scofield, Tanja Slotte</i></p>	<p>6.15 The 1002 <i>Saccharomyces cerevisiae</i> genomes project: a framework for genome-wide association studies <i>J. Peter, A. Friedrich, M. Chiaria, D. Pflieger, A. Bergstrom, A. Sigwalt, K. Freel, G. Liti, <u>Joseph Schacherer</u></i></p>	<p>11.21 Adaptive Evolution of a Clinal Inversion Polymorphism in <i>Drosophila</i> <i>Martin Kapun, C. Schmidt, J. Goudet, P. Schmidt, T. Flatt</i></p>
15:30	<p>22.26 Association mapping reveals the role of mutation-selection balance in maintaining genomic variation for gene expression. <i>Emily Josephs, Y. Lee, J. Stinchcombe, S. Wright</i></p>	<p>6.16 Genetics of Jaw Divergence in a Tropically Polymorphic Cichlid Fish <i>C. Darrin Hulsey</i></p>	<p>11.22 Spatially explicit analysis of harbor porpoise (<i>Phocoena phocoena</i>) genome-wide SNPs improves population resolution in North and Baltic Seas <i>Ljerka Lah, D. Trense, P. Gunnlaugsson, C. Lockyer, U. Siebert, H. Benke, A. Roos, I. Pawliczka, K. Skóra, S. Lourido, B. Öztürk, A. Öztürk, P. Berggren, G. Vikingsson, R. Tiedemann</i></p>
15:45-16:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Early Afternoon, Thursday, July 16th

Time	Prinz Eugen	Ratstube	Notes
	20 Evolution of molecular pathways and networks: Molecular evolution meets systems biology (contin.)	28 The golden age of Archaea: unveiling the diversity and evolution of the third Domain of Life	
14:15	20.11 Adaptive origin of the genetic robustness of metabolic fluxes <i>Wei-Chin Ho, J. Zhang</i>	28.1 From enigmatic curios to global players: current understanding of the diversity and unique contribution of Archaea to global biogeochemical cycles <i>Graeme Nicol</i>	
14:30	20.12 Evolution of Hierarchy in Bacterial Metabolic Networks <i>Aaron Goodman, D. Rhodes, L. Groenendaal, M. Feldman</i>		
14:45	20.13 Reconstruction of ancestral metabolic networks reveals evolutionary gene-reaction-phenotype clustering in the <i>E. coli</i> pangenome <i>TY Pang, M. Lercher</i>	28.2 New approaches to rooting the archaeal radiation <i>Tom A. Williams, S. Heaps, S. Cherlin, T. Nye, R. Boys, T. Embley</i>	
15:00	20.14 Evolution of bow-tie architectures in biology <i>Tamar Friedlander, A. Mayo, T. Tlustý, U. Alon</i>	28.3 Evolutionary history of adaptation to environmental temperature in Archaea <i>Manolo Gouy</i>	
15:15	20.15 High-throughput methods reveal Evolutionary Dynamics of the core regulatory networks in placental mammals <i>Mauris Nnamani, K. Kin, C. Liang, G. Wagner</i>	28.4 Phylogenomic rooting of the domain Archaea: taxonomic and evolutionary implications <i>David Moreira, C. Petitjean, P. Deschamps, P. Lopez-Garcia</i>	
15:30	20.16 The interplay of gene regulatory network structure and evolutionary rate across different time and spatial scales. <i>Angela Early, A. Clark</i>	28.5 "Lokiarchaeum, a novel deep-sea archaeon illuminates the prokaryote to eukaryote transition" <i>Anja Spang, J. Saw, S. Jørgensen, K. Zaremba-Niedzwiedzka, J. Martijn, A. Lind, R. Eijk, C. Schleper, L. Guy, T. Ettema</i>	
15:45-16:15	Coffee Break		

SMBE 2015, Hofburg Vienna, Austria

Late Afternoon, Thursday, July 16th

Time	Festsaal
16:15-17:15	Final Plenary Talk: PI.4 The biology of repetitive DNA: adaptation, epigenetic silencing and aging <i><u>Doris Bachtrog</u></i>
17:15-17:45	Announcement of Prizes, Next Year's SMBE
17:45-18:00	Leave the building